

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 9, 2002, 12:19:35 ; Search time 25.04 Seconds
(without alignments)
34.544 Million cell updates/sec

Title: US-09-759-484-3
Perfect score: 22
Sequence: 1 AMVSE 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	100.0	133	2	09RA22
2	22	100.0	167	5	09VWC3
3	22	100.0	170	2	09Z5U3
4	22	100.0	194	17	097B82
5	22	100.0	201	10	09SRK8
6	22	100.0	202	2	053757
7	22	100.0	202	2	09KWM2
8	22	100.0	202	2	09JRM4
9	22	100.0	202	2	047756
10	22	100.0	202	2	0935Q8
11	22	100.0	214	5	020968
12	22	100.0	215	5	020967
13	22	100.0	238	16	09HYZ1
14	22	100.0	262	16	098FF7
15	22	100.0	326	10	09SNT7
16	22	100.0	345	17	097WV9

17	22	100.0	349	10	09ZQT1	09ZQT1 zea mays (m
18	22	100.0	378	10	09F1A8	09F1A8 arabidopsis
19	22	100.0	398	16	09ZPU2	09ZPU2 rhizobium m
20	22	100.0	406	2	09Z5B7	09Z5B7 streptomyc
21	22	100.0	454	16	09Z5F8	09Z5F8 streptococ
22	22	100.0	457	10	09ZTNG6	09ZTNG6 nicotiana t
23	22	100.0	460	2	006439	006439 rhodobacter
24	22	100.0	474	5	09U298	09U298 caenorhabdi
25	22	100.0	482	12	09O6C0	09O6C0 grapevine 1
26	22	100.0	496	16	09A3R1	09A3R1 caulobacter
27	22	100.0	530	16	09KLC6	09KLC6 vibrio chol
28	22	100.0	533	10	09S1L8	09S1L8 arabidopsis
29	22	100.0	546	2	09KVV28	09KVV28 xanthomonas
30	22	100.0	694	9	09FZR8	09FZR8 mycoplasma
31	22	100.0	768	10	093ZRC3	093ZRC3 arabidopsis
32	22	100.0	787	16	097GMS	097GMS clostridium
33	22	100.0	1056	16	09PAQ0	09PAQ0 xylella fas
34	22	100.0	1119	16	098HG6	098HG6 rhizobium 1
35	22	100.0	1345	10	064496	064496 arabidopsis
36	22	95.5	124	16	099Y57	099Y57 streptococ
37	22	95.5	152	1	033154	033154 methanosarc
38	22	95.5	156	2	095507	095507 pasteurella
39	22	95.5	164	5	09Y0G2	09Y0G2 tetrahymena
40	22	95.5	188	2	09R6M4	09R6M4 agrobacteri
41	22	95.5	200	16	084606	084606 chlamydia t
42	22	95.5	202	2	09F2H8	09F2H8 staphylococ
43	22	95.5	208	16	084365	084365 chlamydia t
44	22	95.5	217	17	097A82	097A82 thermoplas
45	22	95.5	225	8	09B0J0	09B0J0 limodyst

ALIGNMENTS

RESULT 1
ID 09RA22 PRELIMINARY; PRT; 133 AA.
AC 09RA22;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GENES, SIMILAR TO EICOSAPENTAENOIC ACID SYNTHESIS GENE CLUSTER.
OS Vibrio marinus (Moritella marina).
OC Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
OC Moritella.
OX NCBI_TaxID=90736;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MP-1;
RA Tanaka M., Ueno A., Kawasaki K., Yumoto I., Ohguya S., Hoshino T.,
RA Ishizaki K., Okuyama H., Morita N.;
RT "Isolation of clustered genes that are notably homologous to the
RT eicosapentaenoic acid biosynthesis gene cluster from the
RT docosahexaenoic acid-producing bacterium Vibrio marinus strain MP-1.";
RL Biotechnol. Lett. 21:939-945(1999).
DR EMBL: AB025342; BAA89381.1;
DR InterPro: IPR000365; 4HBCOA_thioesterse.
DR Pfam: PF03061; 4HBT.1;
DR PROSITE: PS01328; 4HBCOA_THIOESTERASE; 1.
SQ SEQUENCE 133 AA; 15497 MW; CAB48C641B6D15FC CRC64;

Query Match 100.0%; Score 22; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMVSE 5
|||||
Db 129 AMVSE 133

RESULT 2
09VWC3

ID 09VWC3 PRELIMINARY; PRT; 167 AA.
AC 09VWC3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CG11942 PROTEIN.
GN CG11942.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amaralides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abriil J.F., Adayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu P.V., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertman B.P., Bhandari D., Bolshakov S.,
RA Borrova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Iqbalwam C.,
RA Jalali M., Kalush E., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Misha N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AF003513; AAF49023.1;
DR Flybase: FBgn0031074; CG11942.
DR InterPro: IPR001232; Skp1.
DR Pfam: PF01466; Skp1; 1.
DR SMART: SM00512; Skp1; 1.
DR SMART: SM00512; Skp1; 1.
SQ SEQUENCE 167 AA; 18983 MW; 909E3ED721E6146 CRC64;

Query Match 100.0%; Score 22; DB 5; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMVSE 5
|||||
Db 23 AMVSE 27

RESULT 3
Q92503

ID 092503 PRELIMINARY; PRT; 170 AA.
AC 092503;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE HYPOTHETICAL 19.0 KDA PROTEIN.
OS Zymomonas mobilis.
OC Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
OC Zymomonas.
OX NCBI_Taxid=542;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZM4;
RA Um H.W., Kang H.S.;
RT "Sequence analysis of 41A4 fosmid clone of Zymomonas mobilis.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF124349; AAD19718.1;
KW Hypothetical protein.
SQ SEQUENCE 170 AA; 19008 MW; A4D4496B39AC7140 CRC64;

Query Match 100.0%; Score 22; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMVSE 5
|||||
Db 102 AMVSE 106

RESULT 4
Q97B82 PRELIMINARY; PRT; 194 AA.
AC 097B82;
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE INDOLYTRUVATE FERREDOXIN OXIDOREDUCTASE.
GN TVG0563052.
OS Thermoplasma volcanum.
OC Archaea; Euryarchaeota; Thermoplasmatales; Thermoplasmataceae;
OC Thermoplasma
OX NCBI_Taxid=50339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GSS1 / DSM 4299 / JCM 9571;
RX MEDLINE=20570466; PubMed=11121031;
RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
RA Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
RA Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
RT "Archaeal adaptation to higher temperatures revealed by genomic
RT sequence of Thermoplasma volcanum.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
DR EMBL: AP000992; BAB59717.1;
DR InterPro: IPR002869; POR.
DR Pfam: PF01558; POR; 1.
DR Pyruvate; Complete proteome.
SQ SEQUENCE 194 AA; 20797 MW; 6BA0DEDD38E53647 CRC64;

Query Match 100.0%; Score 22; DB 17; Length 194;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMVSE 5
|||||
Db 168 AMVSE 172

RESULT 5
Q9SRK8 PRELIMINARY; PRT; 201 AA.
ID Q9SRK8
AC Q9SRK8;

DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE F9F8.21 PROTEIN.
 GN F9F8.21.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 NC NCBL_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Lin X., Kaul S., Town C.D., Beilto M., Creasy T.H., Haas B.,
 RA Roming C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
 RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RT "Arabidopsis thaliana chromosome III BAC F9F8 genomic sequence."
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC009991; AAF01524.1; -
 DR EMBL: AC009991; AAF01524.1; -
 DR HSSP: P03012; 2RSL.
 DR InterPro: IPR001822; Recombinase.

Query Match 100.0%; Score 22; DB 10; Length 201;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMVSE 5
 Db 88 AMVSE 92

RESULT 6
 ID 053757 PRELIMINARY; PRT; 202 AA.
 AC 053757;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
 DE RECOMBINASE.
 GN STM.
 OS Staphylococcus aureus, and
 OS Staphylococcus haemolyticus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Staphylococcus.
 NC NCBL_TaxID=1280; 1283;
 RX [1]
 RN SEQUENCE FROM N.A.
 RP SPECIES=S.aureus;
 RC MEDLINE=94215871; PubMed=8163161;
 RA Paulsen I.T., Gillespie M.T., Littlejohn T.G., Hanvivatwong O.,
 RA Rowland S.J., Dyke K.G.H., Skurray R.A.;
 RT "Characterisation of *shm*, a potential recombinase-encoding gene from
 RT *Staphylococcus aureus*."
 RL Gene 141:109-114(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.haemolyticus; STRAIN=NH97A; PLASMID=PNVH97A;
 RA Anthonsen I., Steinhilber T.M., Sidhu M.S., Sundt M.;
 RT "Organization of the beta-lactamase transposon Tn552, the antiseptic
 RT resistant gene *qacA* and a *Staphylococcus* insertion sequence IS257 on
 RT large plasmids in multiresistant *Staphylococcus haemolyticus*."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.aureus; STRAIN=01A1032;
 RA Sutcliffe J.A., Grebe T., Wondrack L., Courvalin P., Cheng J.;
 RT "Partial DNA sequence of *psrL*,"
 RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: L23109; AAA26675.1; -
 DR EMBL: AJ400722; CAB94806.1; -
 DR EMBL: AF167161; AAF99570.1; -
 DR HSSP: P03012; 2RSL.
 DR InterPro: IPR001822; Recombinase.

DR Pfam: PF02796; HTH_7; 1.
 DR Pfam: PF00239; resolvase; 1.
 DR PROSITE: PS00397; RECOMBINASES_1; 1.
 DR PROSITE: PS00398; RECOMBINASES_2; 1.
 KW Plasmid.
 SQ SEQUENCE 202 AA; 23388 MW; BFAA19C46565647 CRC64;

Query Match 100.0%; Score 22; DB 2; Length 202;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMVSE 5
 Db 118 AMVSE 122

RESULT 7
 ID 09KMW2 PRELIMINARY; PRT; 202 AA.
 AC 09KMW2;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE RECOMBINASE.
 OS Staphylococcus warneri.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Staphylococcus.
 NC NCBL_TaxID=1292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sasahara T., Kimura H., Higuchi T., Matsusaki H., Sonomoto K.,
 RA Ishizaki A.;
 RT "Staphylococcus warneri truncated *nukM*, *nuka*, *orf1* genes, and the
 RT downstream region."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kimura H., Matsusaki H., Sasahara T., Sonomoto K., Ishizaki A.;
 RT "Purification and partial identification of bacteriocin ISK-1,"
 RT antibiotic produced by *Pedococcus* sp. ISK-1."
 RL Biosci. Biotechnol. Biochem. 62:2341-2345(1998).
 DR EMBL: AB034941; BAA99388.1; -
 DR HSSP: P03012; 2RSL.
 DR InterPro: IPR001822; Recombinase.
 DR Pfam: PF02796; HTH_7; 1.
 DR Pfam: PF00239; resolvase; 1.
 DR PROSITE: PS00397; RECOMBINASES_1; 1.
 DR PROSITE: PS00398; RECOMBINASES_2; 1.
 SQ SEQUENCE 202 AA; 23549 MW; 1818AV/EFDI6C40BD CRC64;

Query Match 100.0%; Score 22; DB 2; Length 202;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AMVSE 5
 Db 118 AMVSE 122

RESULT 8
 ID 09JRM4 PRELIMINARY; PRT; 202 AA.
 AC 09JRM4;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE B1N3 PROTEIN.
 GN B1N3.
 OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas
 OS maltophilia).
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;

OC Stenotrophomonas.
OX NCBI_TaxID=40324;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D457;
RA Jose M.L.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=D457;
RA MEDLINE=20316786; PubMed=10858330;
RX Alonso A., Sanchez P., Martinez J.L.;
RT "Stenotrophomonas maltophilia D457r contains a cluster of genes from
gram-positive bacteria involved in antibiotic and heavy metal
resistance.";
RL Antituberc. Agents Chemother. 44:1778-1782(2000).
DR EMBL: AJ251015; CAB96927.1; -.
DR HSSP: P03012; 2RSL.
DR InterPro: IPR001822; Recombinase.
DR Pfam: PF02796; HTH_7; 1.
DR PROSITE: PS00397; RECOMBINASES_1; 1.
DR PROSITE: PS00398; RECOMBINASES_2; 1.
SQ SEQUENCE 202 AA; 23480 MW; 24962D8B2E3C92E0 CRC64;

Query Match 100.0%; Score 22; DB 2; Length 202;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AMVSE 5
DB 118 AMVSE 122

RESULT 9
ID Q47756 PRELIMINARY; PRT; 202 AA.
AC Q47756;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE INVERTASE-ENTEROCOCCAL.
GN ENRTIN.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC TRANSPOSON-TNS52 (PARTIAL);
RX MEDLINE=96271183; PubMed=8700969;
RA Rice L.B., Carlas L.L., Marshall S.H., Bonafede M.E.;
RT "Sequences found on staphylococcal beta-lactamase plasmids integrated
into the chromosome of Enterococcus faecalis CH116.";
RL Plasmid 35:81-90(1996).
DR EMBL: U39859; AAB08926.1; -.
DR HSSP: P03012; 2RSL.
DR InterPro: IPR001822; Recombinase.
DR Pfam: PF02796; HTH_7; 1.
DR PROSITE: PS00397; RECOMBINASES_1; 1.
DR PROSITE: PS00398; RECOMBINASES_2; 1.
SQ SEQUENCE 202 AA; 23504 MW; 060B4E50EA82E08C CRC64;

Query Match 100.0%; Score 22; DB 2; Length 202;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AMVSE 5
DB 118 AMVSE 122

RESULT 10
ID Q93S08 PRELIMINARY; PRT; 202 AA.
AC Q93S08;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RECOMBINASE SIN.
GN SIN.
OS Staphylococcus epidermidis.
OG Plasmid PST6.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=6;
RA Sidhu M.S., Heir E., Sorum H., Holck A.L.;
RT "Genetic linkage between quaternary ammonium compound and beta-lactam
resistance in Staphylococci isolated from food.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF028779; AAK38455.1; -.
KW Plasmid.
SQ SEQUENCE 202 AA; 23402 MW; 2E4E027C8CE21442 CRC64;

Query Match 100.0%; Score 22; DB 2; Length 202;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AMVSE 5
DB 118 AMVSE 122

RESULT 11
ID Q20968 PRELIMINARY; PRT; 214 AA.
AC Q20968;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE F58B3.3 PROTEIN.
GN F58B3.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OX Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Harris B.R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL: Z73427; CAA97801.1; -.
SQ SEQUENCE 214 AA; 23089 MW; FA1992EC471FF165 CRC64;

Query Match 100.0%; Score 22; DB 5; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AMVSE 5
DB 131 AMVSE 135

RESULT 12
Q20967 PRELIMINARY; PRT; 215 AA.
AC Q20967;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
GN F58B3.2 PROTEIN.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Harris B.R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL: 273427; CAAG7800.1;
SO SEQUENCE 215 AA; 23528 MW; 026249629A61DD7C CRC64;

Query Match
Best Local Similarity 100.0%; Score 22; DB 5; Length 215;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5
Db 132 AMVSE 136

RESULT 13
Q9HYZ1 PRELIMINARY; PRT; 238 AA.
AC Q9HYZ1;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
GN PROBABLE TRANSCRIPTIONAL REGULATOR.
PA3249.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stoyer C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Barody L.L., Coulter S.N., Folger K.R., Kas A., Lardig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reiter J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -1. SIMILARITY: BELONGS TO THE GNTR FAMILY OF TRANSCRIPTIONAL
REGULATORS.
DR EMBL: AE004747; AAC06637.1;
DR InterPro: IPR000524; HTH_GNTR.
DR Pfam: PF00392; gntR.1.
DR PRINTS: PR00035; HTHGNTR.
DR SMART: SM00345; HTH_GNTR.1.
DR PROSITE: PS00043; HTH_GNTR_FAMILY.1.
KW Complete proteome; DNA-binding; Transcription regulation.

SQ SEQUENCE 238 AA; 26802 MW; 1DAEB7F680EE7F10 CRC64;

Query Match
Best Local Similarity 100.0%; Score 22; DB 16; Length 238;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5
Db 88 AMVSE 92

RESULT 14
Q98FF7 PRELIMINARY; PRT; 262 AA.
AC Q98FF7;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DE 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
GN TRANSCRIPTIONAL REGULATOR.
ML3795.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asanizu E., Kato T., Sasamoto S.,
Matenabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL: AP003002; BAB50610.1;
DR InterPro: IPR000285; HTH_ICLR.
DR Pfam: PF01614; ICLR.1.
DR ProDom: PD002768; HTH_ICLR.1.
KW Complete proteome.
SQ SEQUENCE 262 AA; 28425 MW; 9FD618A4D360D8CF CRC64;

Query Match
Best Local Similarity 100.0%; Score 22; DB 16; Length 262;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AMVSE 5
Db 170 AMVSE 174

RESULT 15
Q9SNL7 PRELIMINARY; PRT; 326 AA.
AC Q9SNL7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
GN SIMILAR TO MAGNESIUM-PROTOPORPHYRIN IX METHYLTRANSFERASE (PUTATIVE
MAGNESIUM-PROTOPORPHYRIN IX METHYLTRANSFERASE).
P0679C08.13.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriocarpaceae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPOBARE;
DR Sasaki T., Matsumoto T., Yamamoto K.;

Tue Jul 9 13:40:25 2002

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Page 6

RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
RT clone: P0493C11.1;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, NIPPONBARE;
RA Saeki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
RT clone: P0679C06.1;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP000559; BAA84812.1; -
DR EMBL; AP002542; BAB19374.1; -
DR InterPro: IPR000051; SAM_bind.
KW Transferase: Methyltransferase.
SQ SEQUENCE 326 AA; 34926 MW; F8C91146F172278 CRC64;

Query Match 100.0%; Score 22; DB 10; Length 326;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AMYSE 5
|||||
Db 182 AMYSE 186

Search completed: July 9, 2002, 12:23:04
Job time: 209 sec